

# SEQUENCE ALIGNMENT -

SEQ ID NO: 2 VS. SEQ ID NO: 4

GenCore version 5.1.4\_p5\_4578  
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OM protein - protein search, using sw model

Run on: May 5, 2003, 11:48:53 ; Search time 1 Seconds  
(without alignments)  
4.471 Million cell updates/sec

Title: us-10-090-516-4  
Perfect score: 8858  
Sequence: 1 MDVKERKPYRSLTRRRDAER.....ITDNNNGNMVNVRDSTGMPL 1624

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.0

Searched: 1 seqs, 2753 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1 summaries

Database : us-10-090-516-2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB Length	ID	Description
1	8858	100.0	2753	1	us-10-090-516-2	

## ALIGNMENTS

RESULT 1  
us-10-090-516-2

Query Match 100.0%; Score 8858; DB 1; Length 2753;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1624; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MDVKERKPYRSLTRRRDAERRY	TSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV	60
Db	1	MDVKERKPYRSLTRRRDAERRY	TSSSADSEEGKAPQKSYSSSETLKAYDQDARLAYGSRV	60
Qy	61	KDIVPQEAEFCRTGANFTLRELGL	EEVTPPHGTLYRTDIGLPHCGYSMGAGSDADMEAD	120
Db	61	KDIVPQEAEFCRTGANFTLRELGL	EEVTPPHGTLYRTDIGLPHCGYSMGAGSDADMEAD	120
Qy	121	TVLSPEHPVRLWGRSTRSGRSSCL	SSRANSNLTLTDEHENTETDHPGGLQNHARLRTPP	180
Db	121	TVLSPEHPVRLWGRSTRSGRSSCL	SSRANSNLTLTDEHENTETDHPGGLQNHARLRTPP	180
Qy	181	PPLSHAHTPNQHHAAASINSLNR	GNFTPRSNPSPAPTDHSLSGEPPAGGAQEPAAHQENWL	240
Db	181	PPLSHAHTPNQHHAAASINSLNR	GNFTPRSNPSPAPTDHSLSGEPPAGGAQEPAAHQENWL	240
Qy	241	LNSNIPLETRNLGKQPFGLTQDN	LIEMDILGASRHDGAYS DGHFLFKPGGTSPLFCTTS	300

Db 241 LNSNIPLETRNLGKQPFLGTLQDNLIEMDILGASRHDGAYSDGHFLFKPGGTSPLFCTTS 300  
 Qy 301 PGYPLTSSTVYSPPPRPLPRSTFARPAFNLKKPSKYNWKAALSAIVISATLVILLAYF 360  
 Db 301 PGYPLTSSTVYSPPPRPLPRSTFARPAFNLKKPSKYNWKAALSAIVISATLVILLAYF 360  
 Qy 361 VAMHLFGLNWLQPMEGQMYEITEDTASSWPVPTDVSLYPSGGTGLETDPDRKGKGTTEGK 420  
 Db 361 VAMHLFGLNWLQPMEGQMYEITEDTASSWPVPTDVSLYPSGGTGLETDPDRKGKGTTEGK 420  
 Qy 421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIDHPVHLKFNVSLGKAALVGIYG 480  
 Db 421 PSSFFPEDSFIDSGEIDVGRRASQKIPPGTFWRSQVFIDHPVHLKFNVSLGKAALVGIYG 480  
 Qy 481 RKGLPPSHTQFDFVELLDGRRLLTQEARSLGTPRQSRGTVPSSHETGFIQYLDSGIWH 540  
 Db 481 RKGLPPSHTQFDFVELLDGRRLLTQEARSLGTPRQSRGTVPSSHETGFIQYLDSGIWH 540  
 Qy 541 LAFYNDGKESEVVSFLTTAIESVDNCPSNCGNGDCISGTCHCFLGFLGPDGGRASCPVL 600  
 Db 541 LAFYNDGKESEVVSFLTTAIESVDNCPSNCGNGDCISGTCHCFLGFLGPDGGRASCPVL 600  
 Qy 601 CSGNGQYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTCTITGTCICNPGYKGESCEEV 660  
 Db 601 CSGNGQYMKGRCLCHSGWKGAECDVPTNQCIDVACSNHGTCTITGTCICNPGYKGESCEEV 660  
 Qy 661 DCMDPTCSGRGVCVRGECHCSVGWGGTNCETPRATCLDQCSGHGTFLPDTGLCSCDPSWT 720  
 Db 661 DCMDPTCSGRGVCVRGECHCSVGWGGTNCETPRATCLDQCSGHGTFLPDTGLCSCDPSWT 720  
 Qy 721 GHDCSIEICAADCGGHGVCVGGTCCRCDGWMGAACDQRACHPRCAEHGTCRDGKCECSPG 780  
 Db 721 GHDCSIEICAADCGGHGVCVGGTCCRCDGWMGAACDQRACHPRCAEHGTCRDGKCECSPG 780  
 Qy 781 WNGEHTIEGCPGLCNGNGRCTLDLNGWHVCVQLGWRGAGCDTSMETACGDSKDNDGDGL 840  
 Db 781 WNGEHTIEGCPGLCNGNGRCTLDLNGWHVCVQLGWRGAGCDTSMETACGDSKDNDGDGL 840  
 Qy 841 VDCMDPDCCQLPLCHINPLCLGSPNPLDIIQETQVPVSQQNLHSFYDRIKFLVGRDSTHI 900  
 Db 841 VDCMDPDCCQLPLCHINPLCLGSPNPLDIIQETQVPVSQQNLHSFYDRIKFLVGRDSTHI 900  
 Qy 901 IPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFVNNPLFGYTIISRQDGSFDLVTNGGIS 960  
 Db 901 IPGENPFDGGHACVIRGQVMTSDGTPLVGVNISFVNNPLFGYTIISRQDGSFDLVTNGGIS 960  
 Qy 961 IILRFERAPFITQEHTLWLPWDRFFVMEIIMRHEENEIPSCDLSNFARNPNVVSPLT 1020  
 Db 961 IILRFERAPFITQEHTLWLPWDRFFVMEIIMRHEENEIPSCDLSNFARNPNVVSPLT 1020  
 Qy 1021 SFASSCAEKGPVPEIQALQEEISISGCKMRLSYLSSRTPGYKSVLRISLTHPTIPFNL 1080  
 Db 1021 SFASSCAEKGPVPEIQALQEEISISGCKMRLSYLSSRTPGYKSVLRISLTHPTIPFNL 1080  
 Qy 1081 KVHLMVAVEGRLFRKWFAAAPDLSYFIWDKTDVYNQKVFLSEAFVSVGYEYESCPDLI 1140  
 Db 1081 KVHLMVAVEGRLFRKWFAAAPDLSYFIWDKTDVYNQKVFLSEAFVSVGYEYESCPDLI 1140  
 Qy 1141 LWEKRTTVLQGYEIDASKLGGWSLDKHHALNIQSGILHKGNGENQFVSQQPPVIGSIMGN 1200  
 Db 1141 LWEKRTTVLQGYEIDASKLGGWSLDKHHALNIQSGILHKGNGENQFVSQQPPVIGSIMGN 1200  
 Qy 1201 GRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIFFPSGNVTNILELSHS 1260  
 Db 1201 GRRRSISCPSCNGLADGNKLLAPVALTCGSDGSLYVGDFNYIRRIFFPSGNVTNILELSHS 1260  
 Qy 1261 PAHKYYLATDPMGAVFLSDSNSRRVFKIKSTVVVKDLVKNSEVVAGTGDQCLPFDDTRC 1320  
 Db 1261 PAHKYYLATDPMGAVFLSDSNSRRVFKIKSTVVVKDLVKNSEVVAGTGDQCLPFDDTRC 1320  
 Qy 1321 GDGGKATEATLTNPRGITVDKFLIYFVDGTMIRRIDQNGIISTLLGSNDLTSARPLSCD 1380

